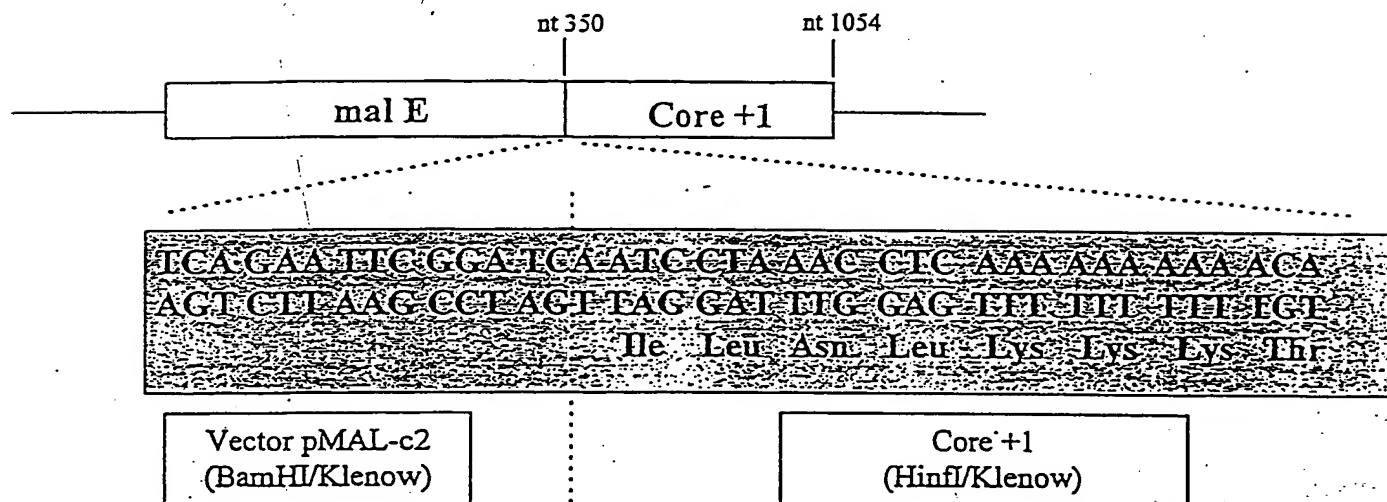


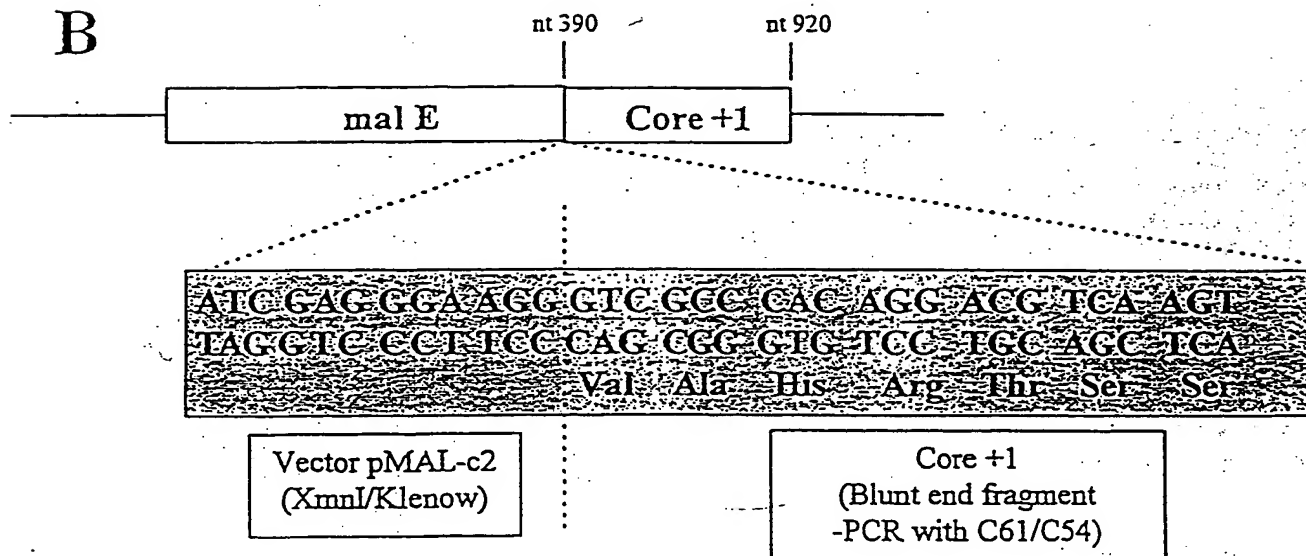
MalE-CORE+1 RECOMBINANT PROTEINS

A



pHPI 643

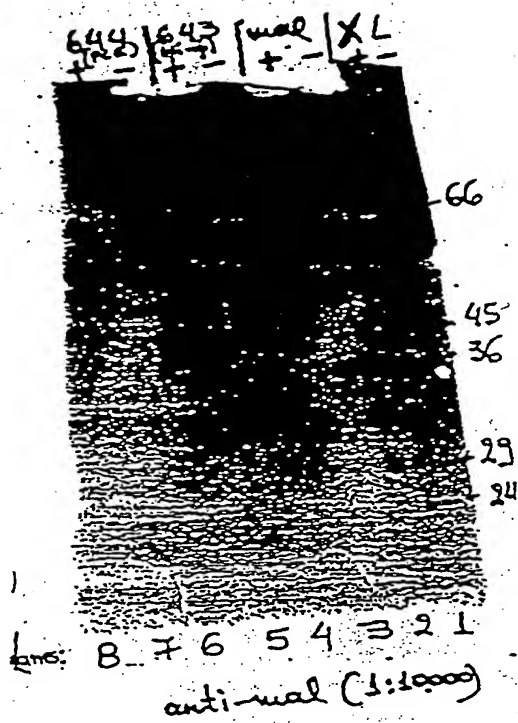
B



pHPI 644

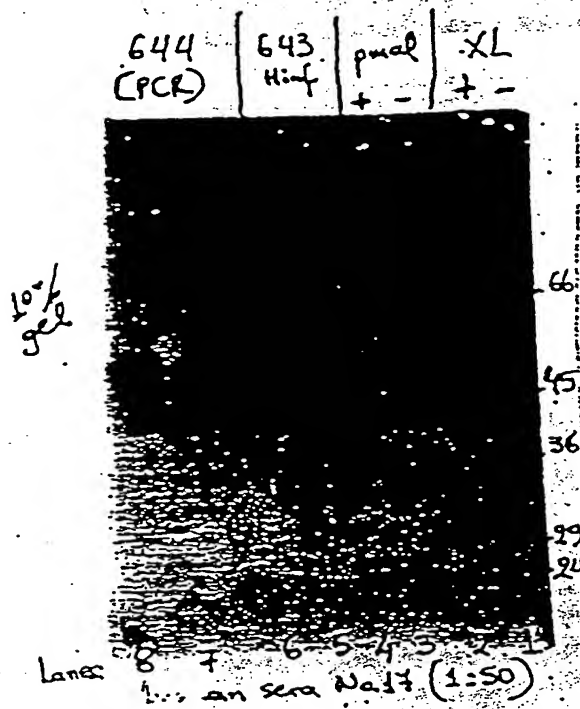
FIGURE 1

Panel A



10% gel

Panel B



10% gel

Figure 2

Panel A

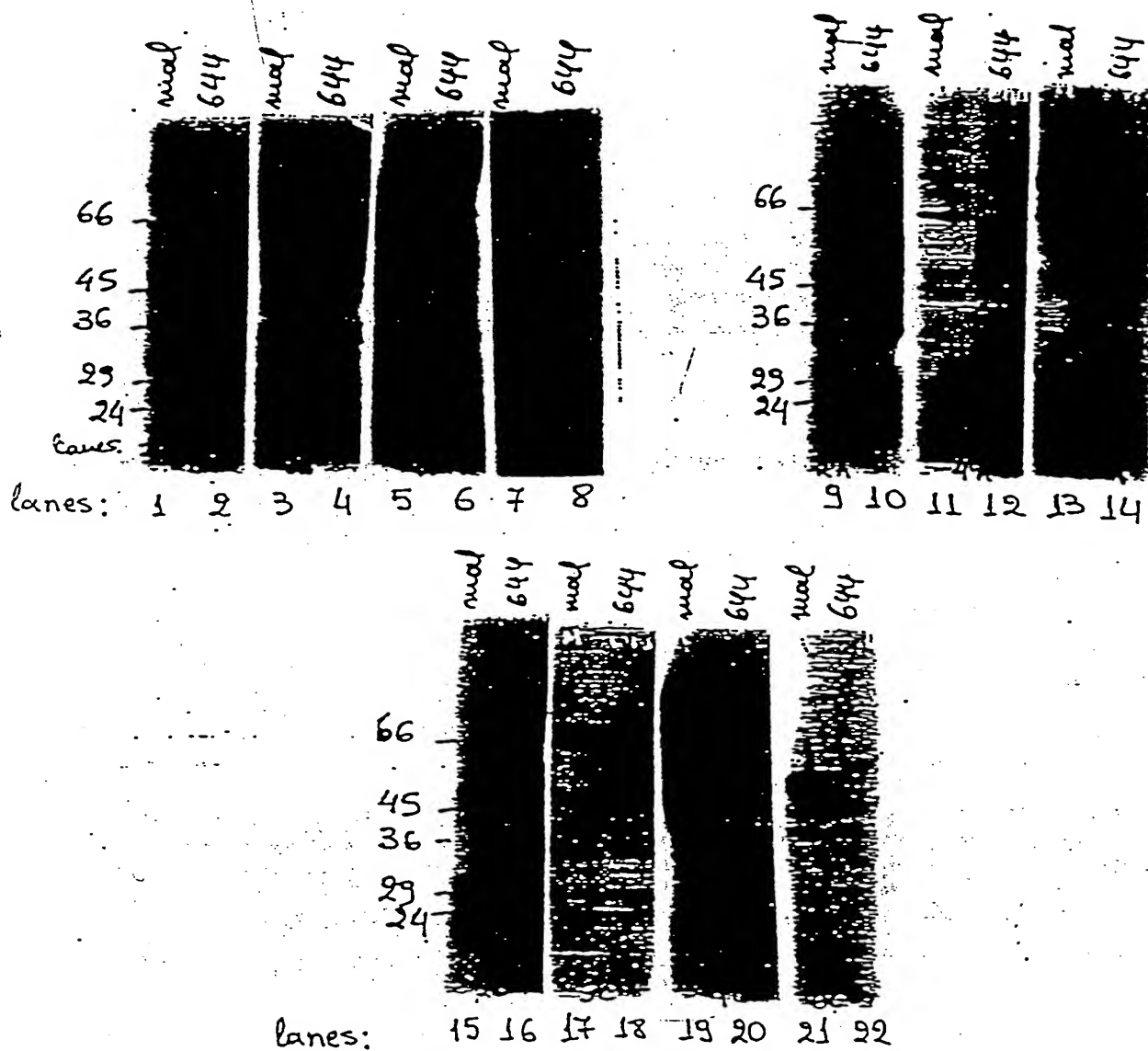


Figure 3

Panel B

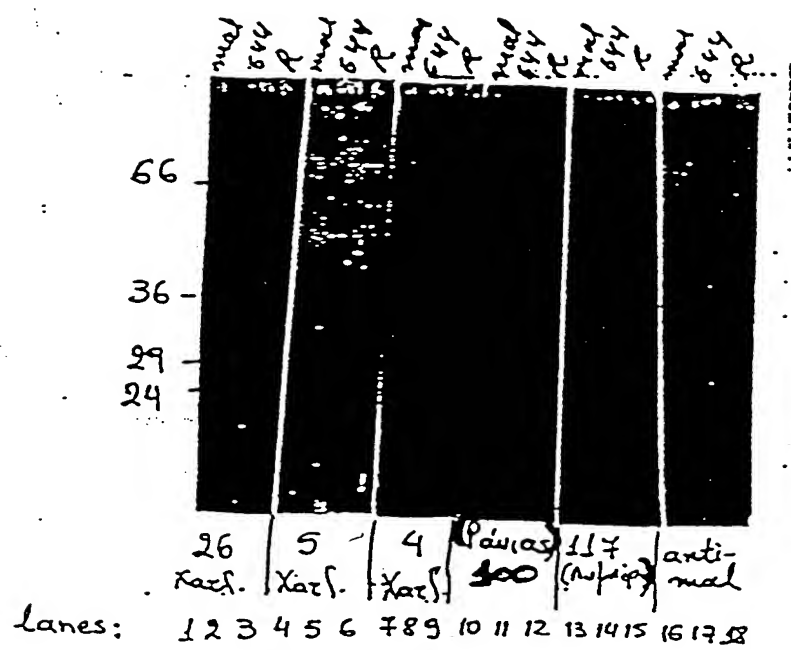
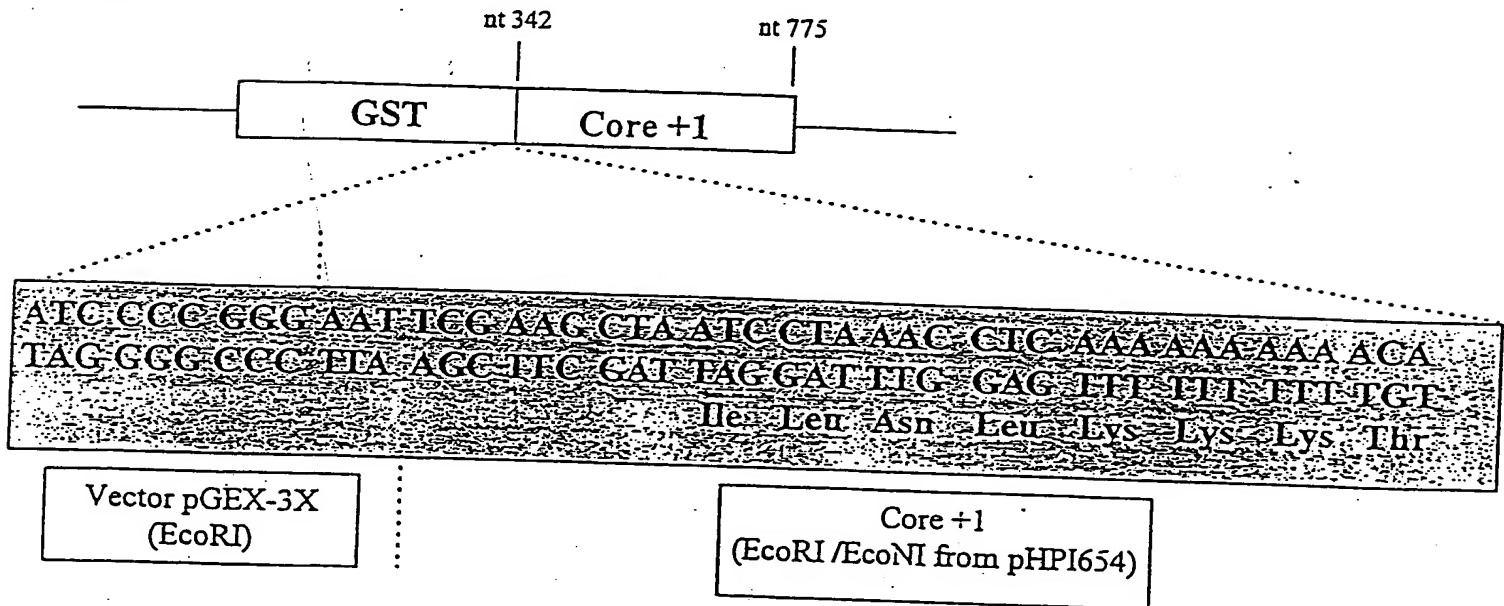


Figure 3 (cont.)

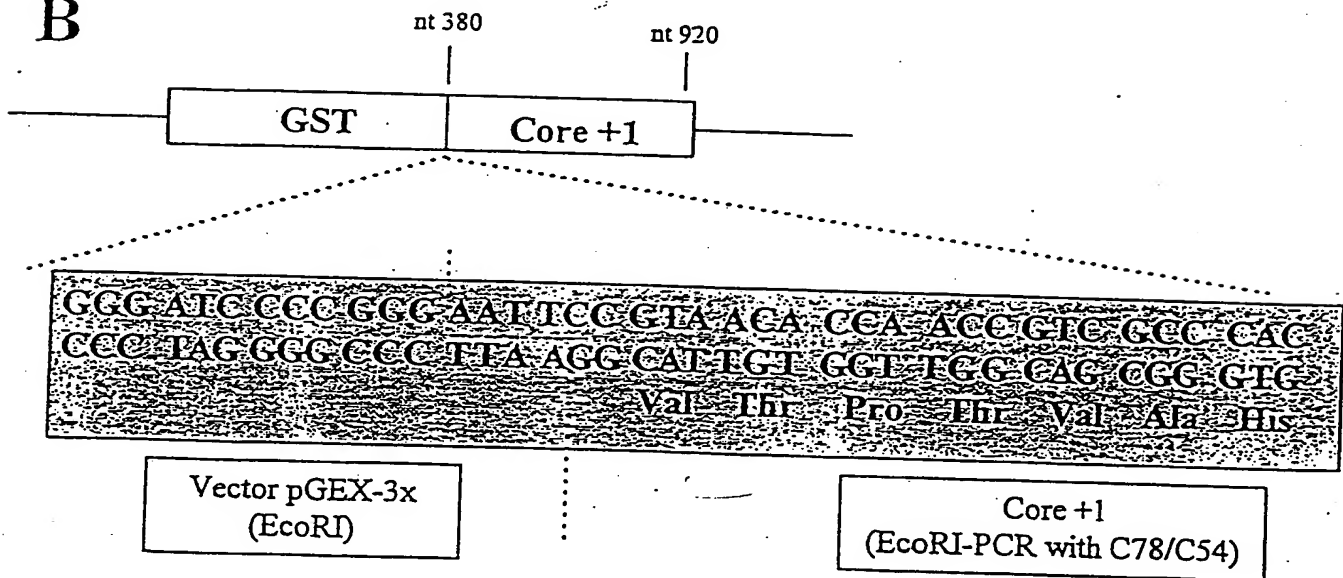
GST-CORE+1 RECOMBINANT PROTEINS

A



pHPI 663

B



pHPI 668

FIGURE 4

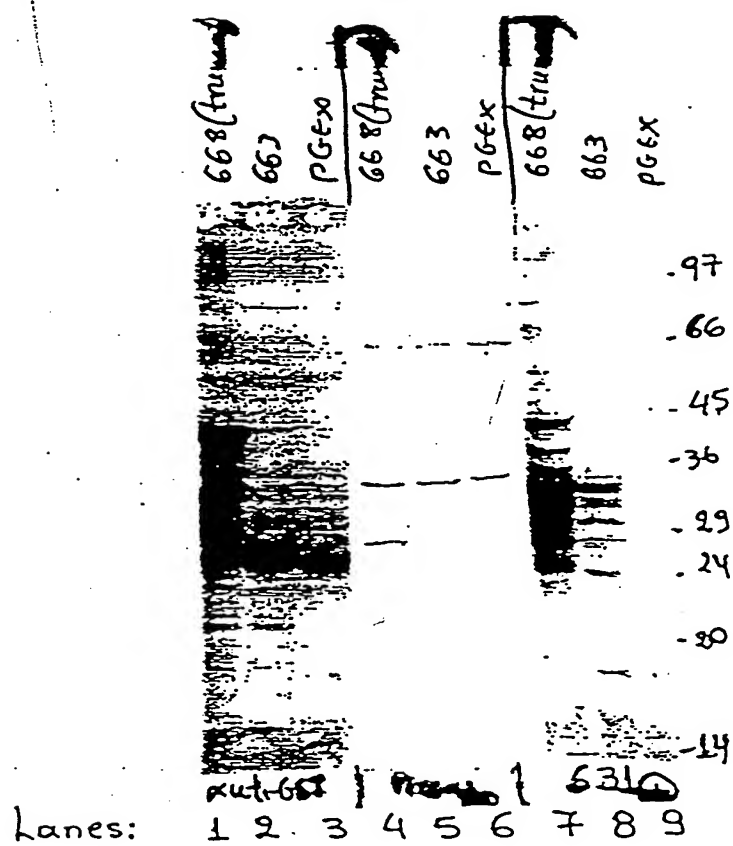


Figure 5

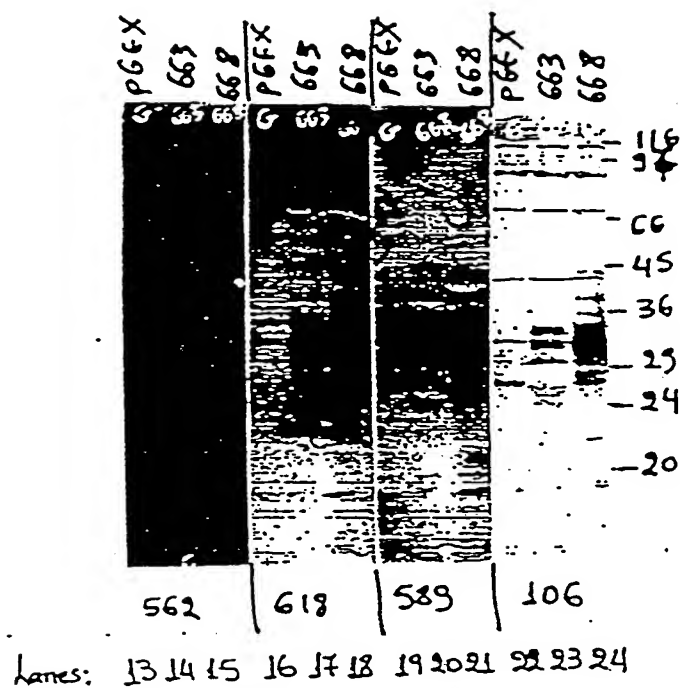
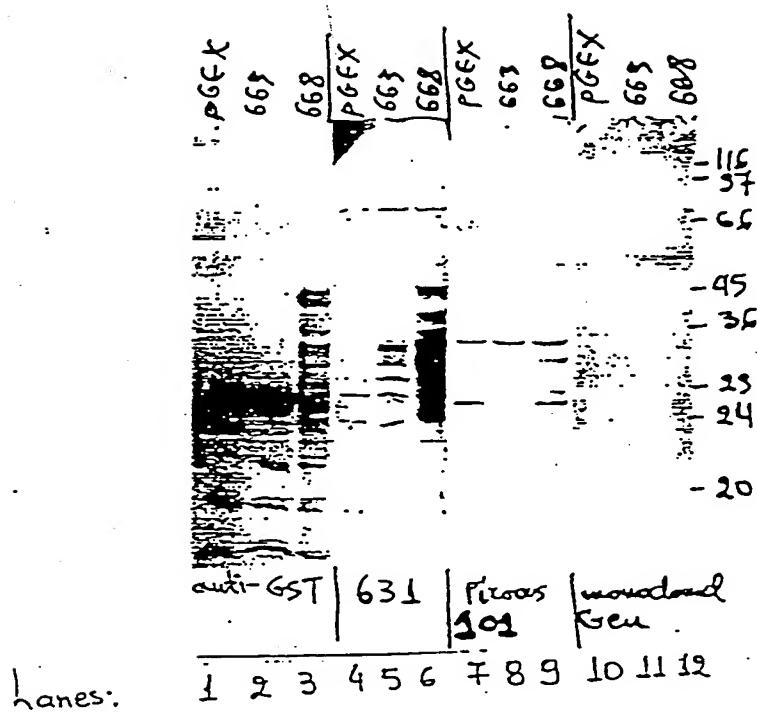


Figure 6

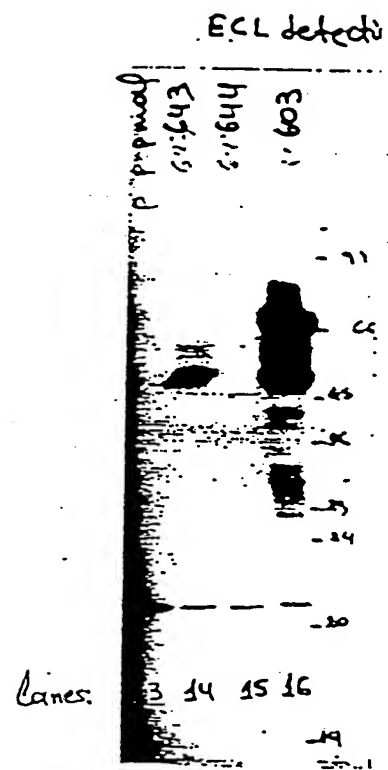
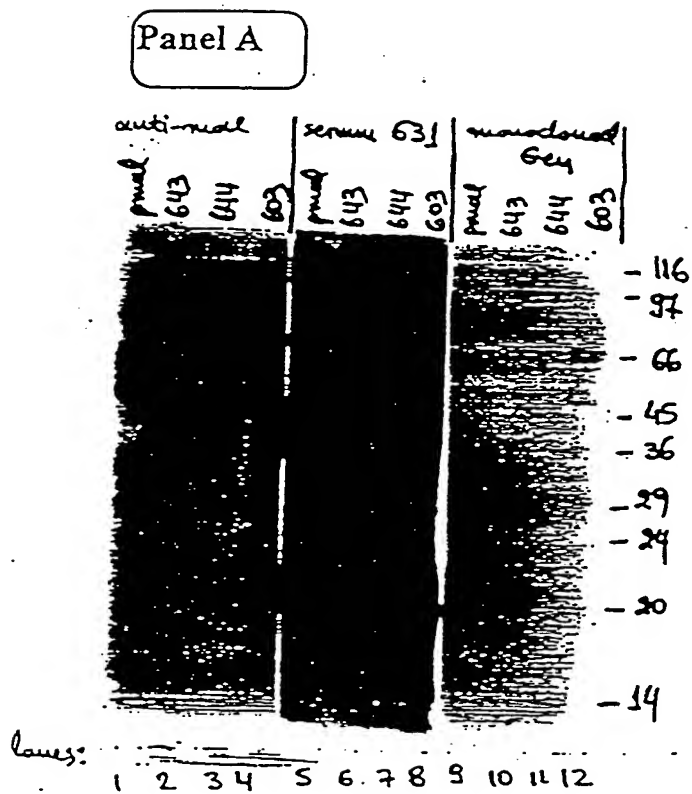
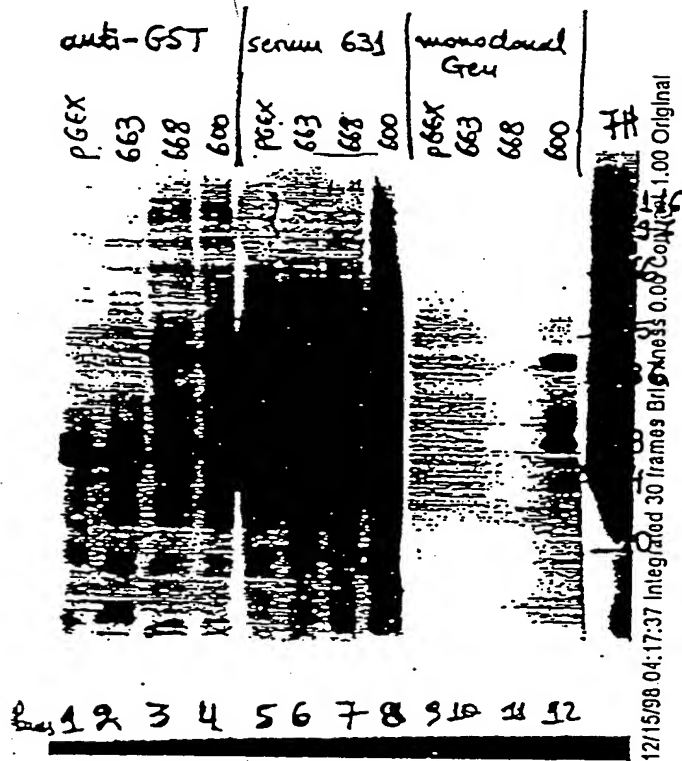


Figure 7

Panel B



lanes: 13 14 15 16

Figure 7 (Cont.)

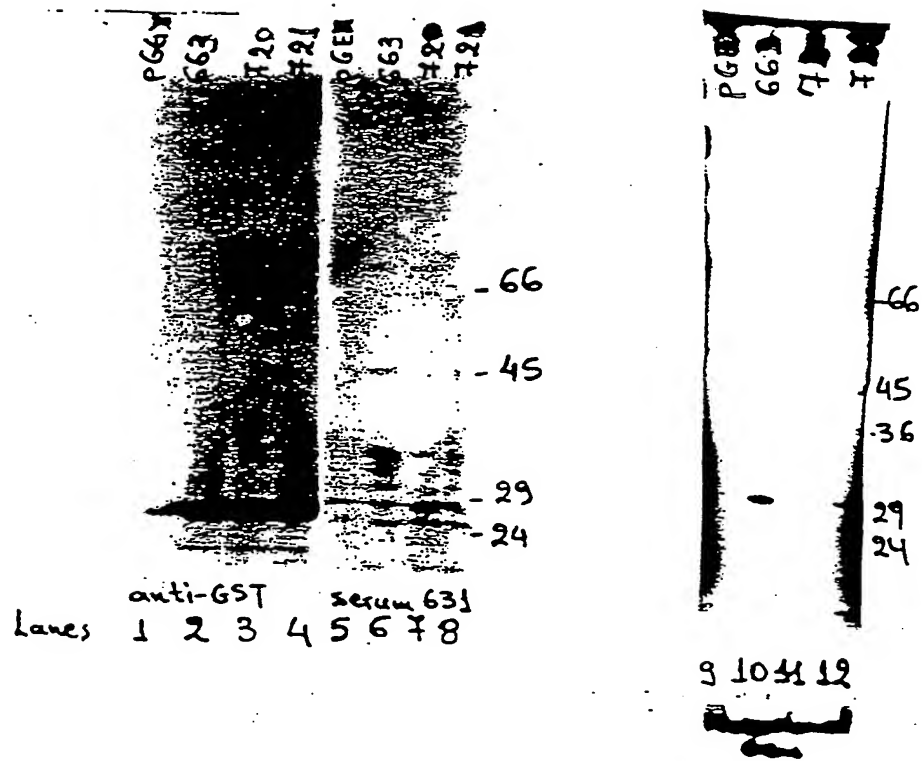


Figure 8

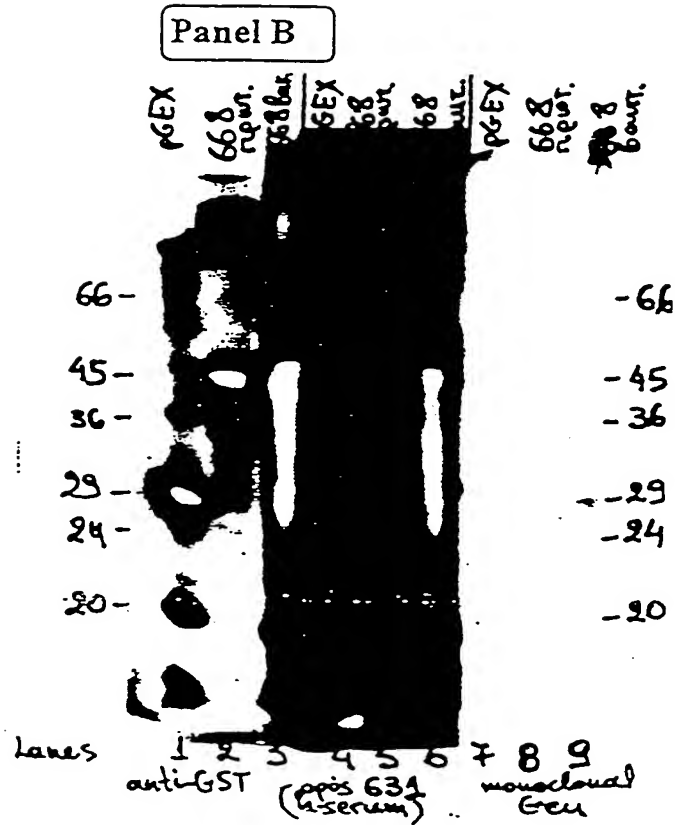
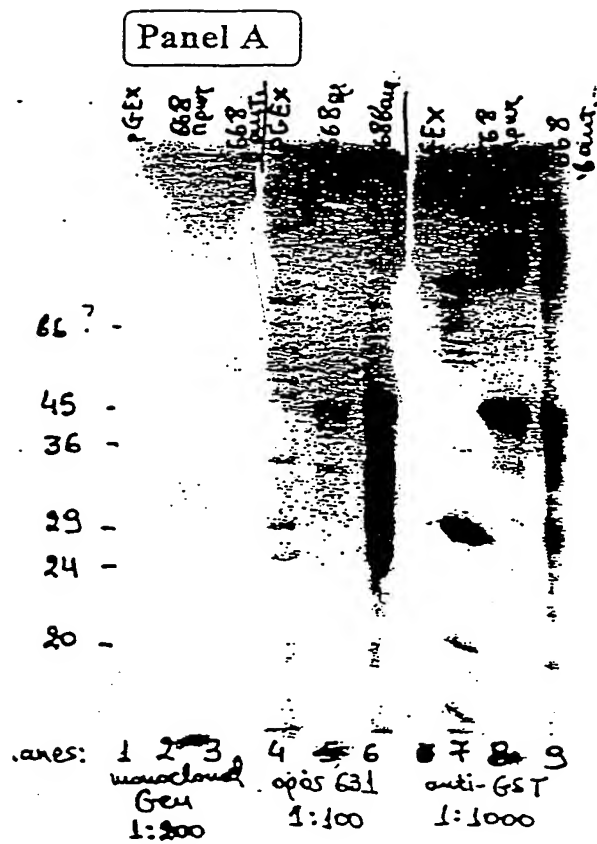


Figure 9

Panel C

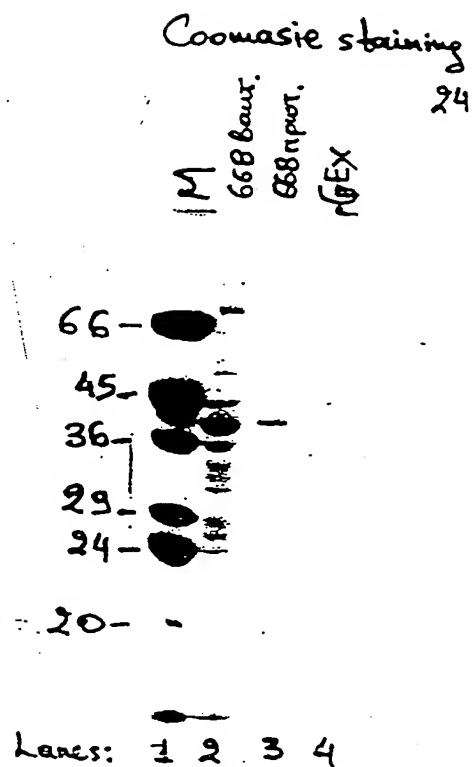


Figure 9 (cont.)

Wild type
pHPI 643 &
pHPI 663

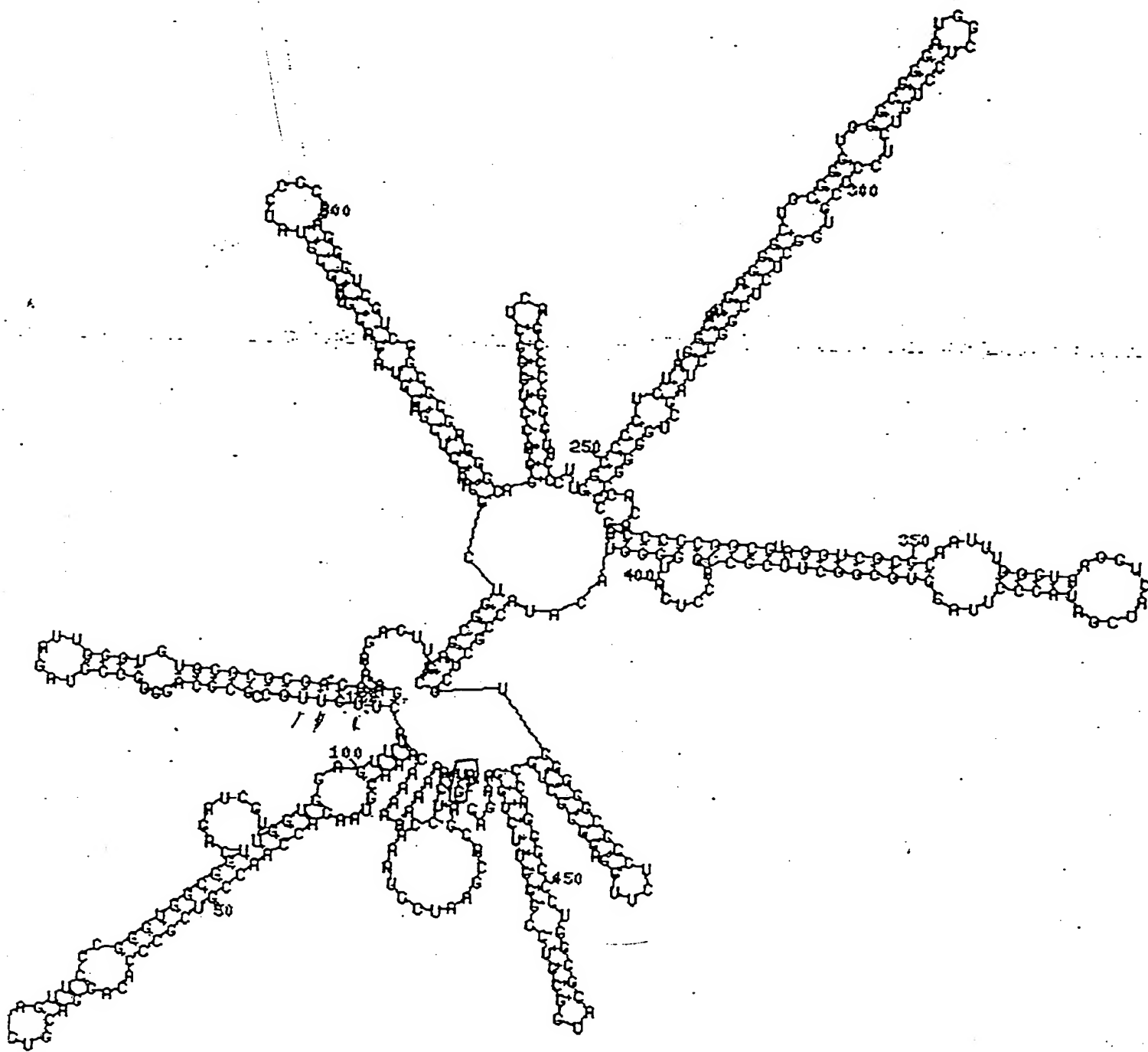


Figure 10 a

f by D. Stewart and M. Zuker

Washington University

His → Leu

pHPI 676

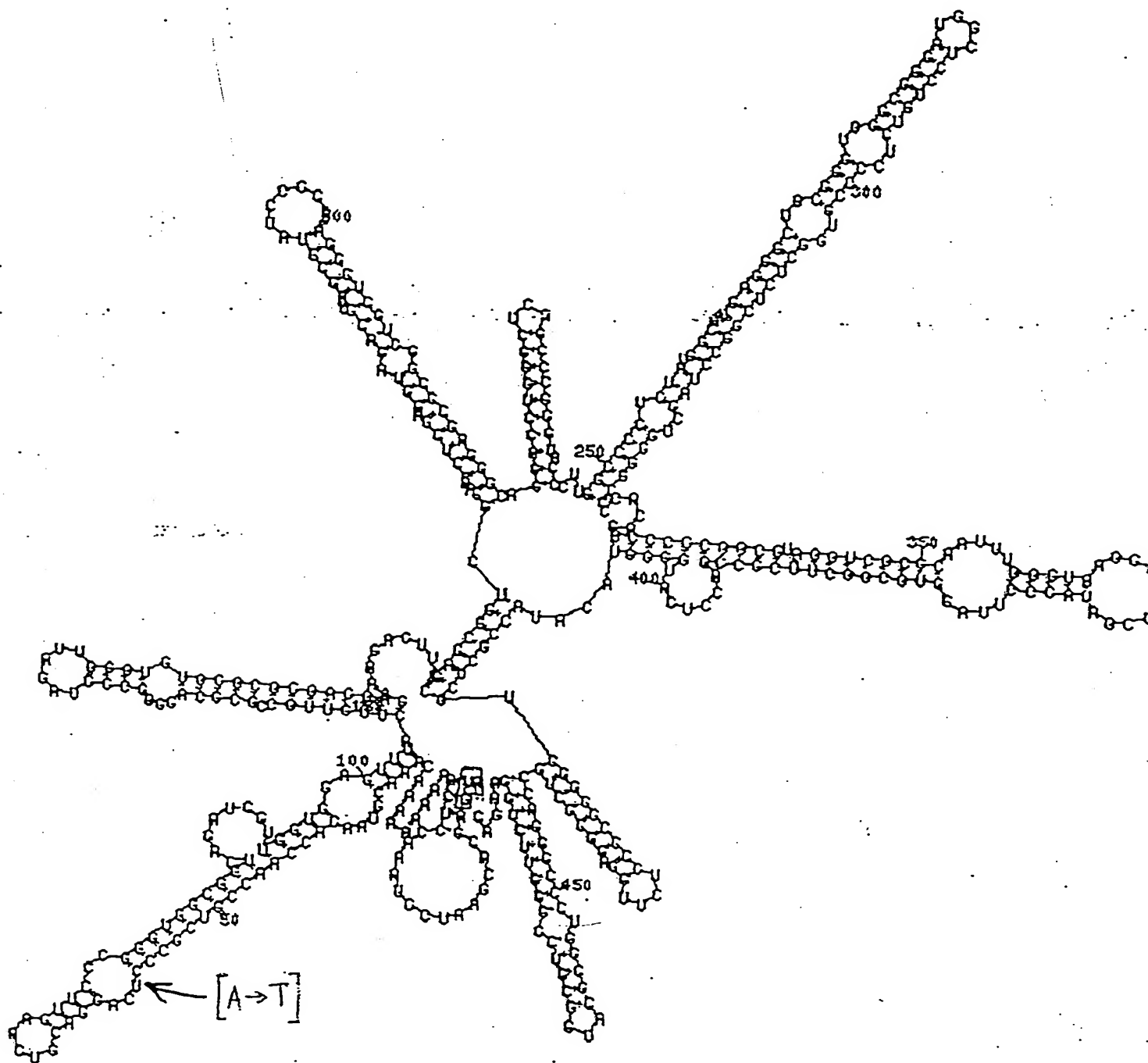


Figure 10 b

Cys → Ser.
pHPI 679

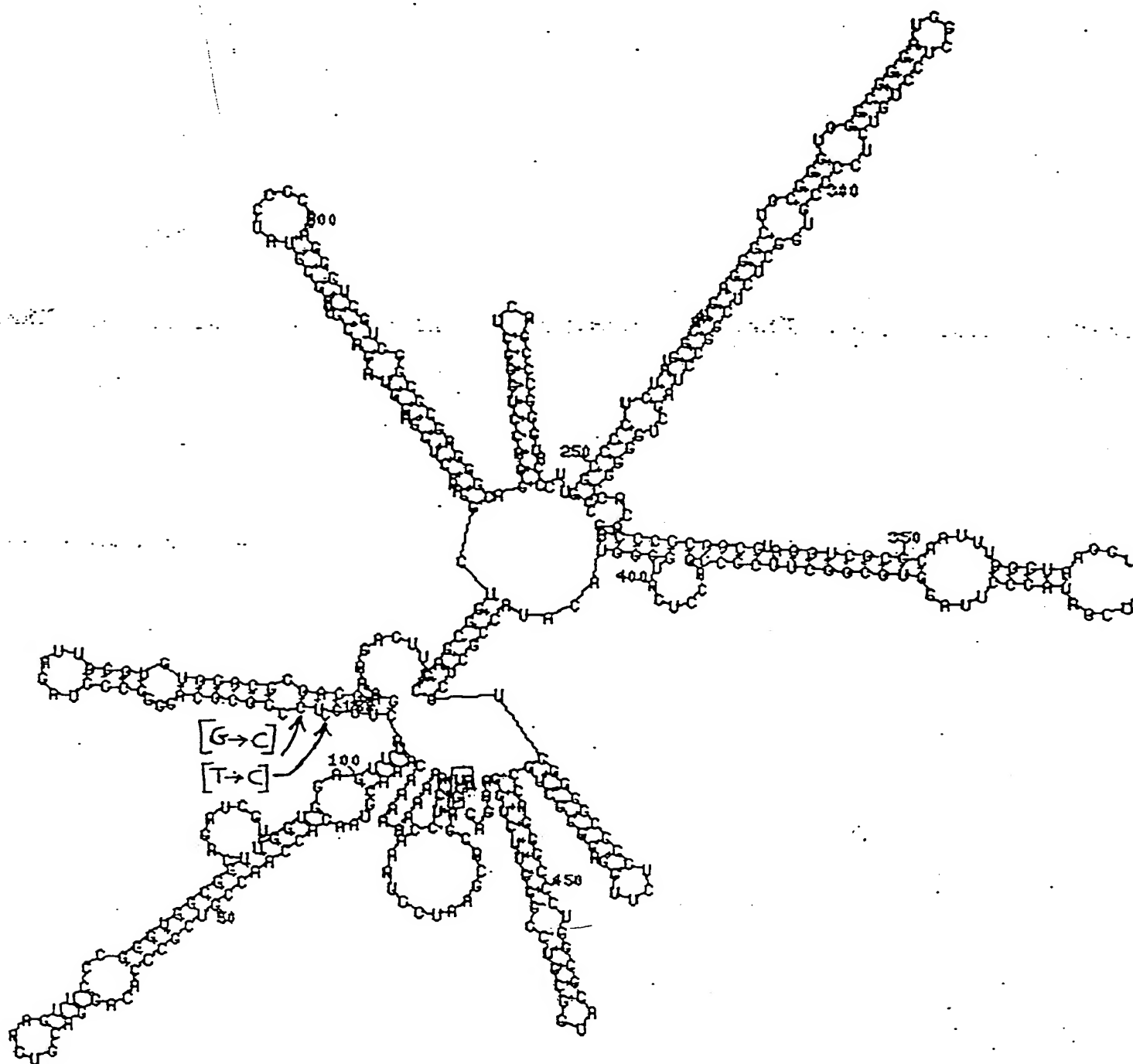


Figure 10 c

His \rightarrow Leu & Cys \rightarrow Ser
pHPI 719

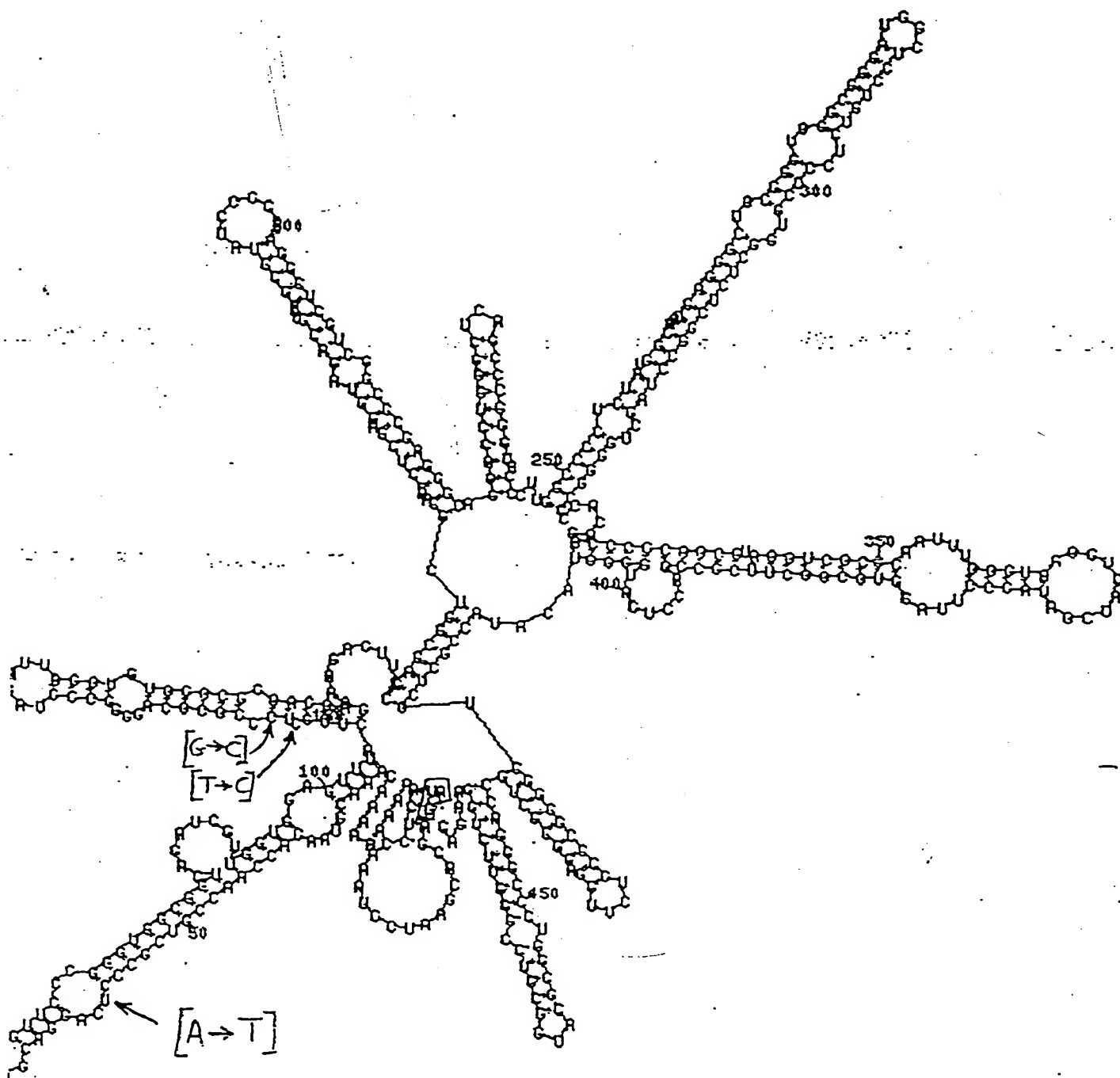


Figure 10 d

Cys-Cys \rightarrow Gly-Gly
pHPI 720

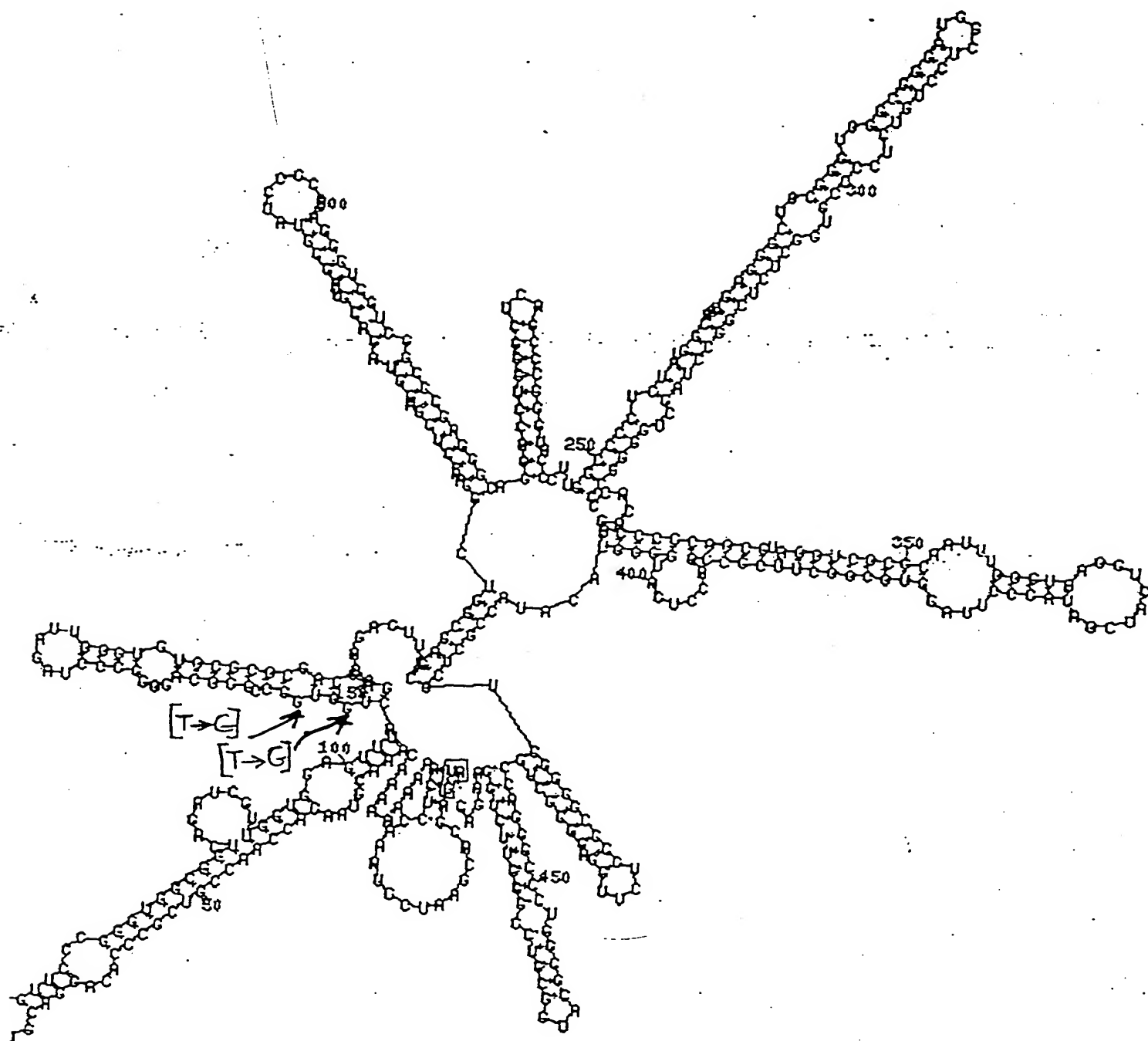
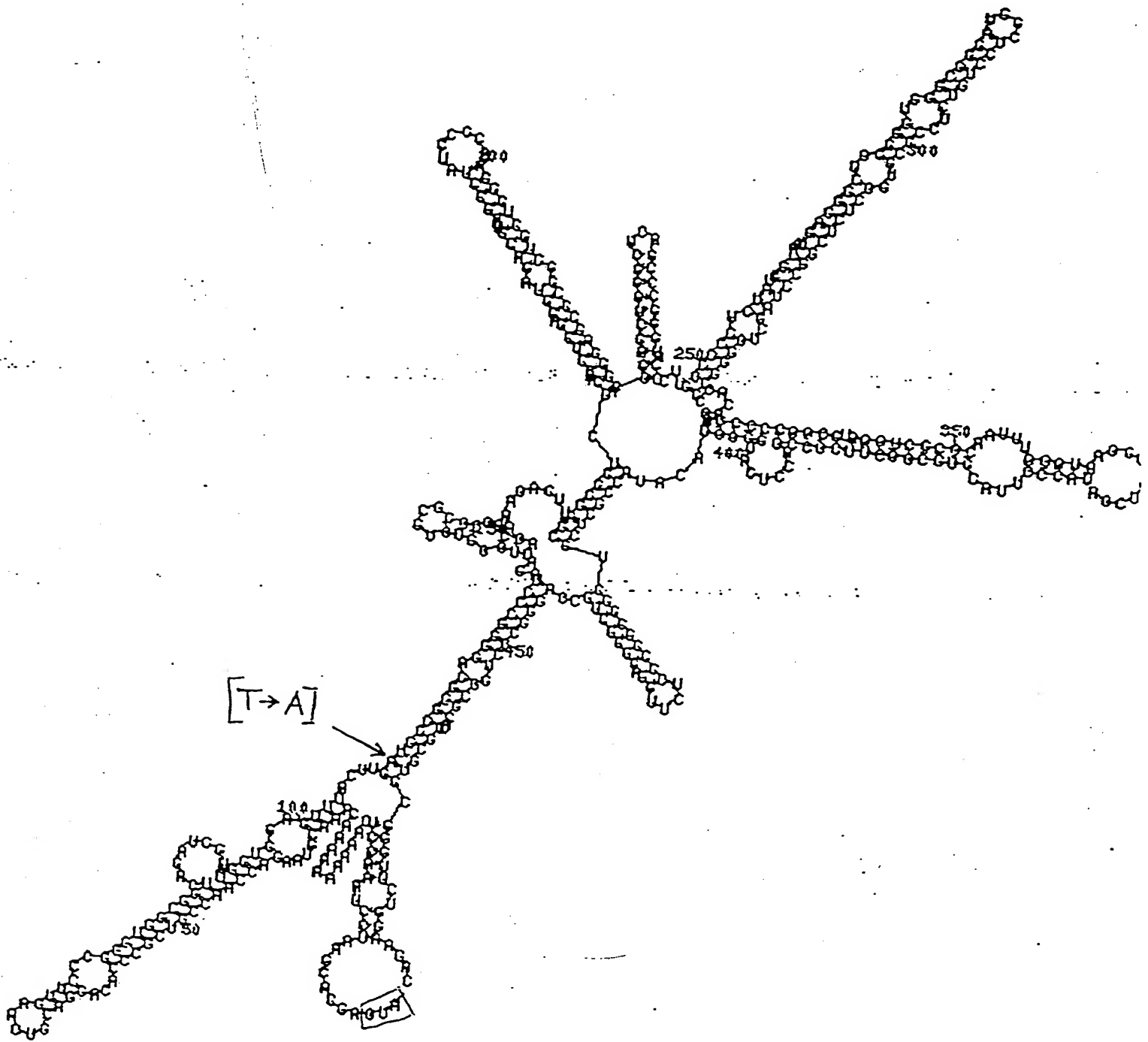


Figure 10 e

Cys → stop codon
pHPI 721



ENERGY = -236.1 [initially...]

Figure 10f

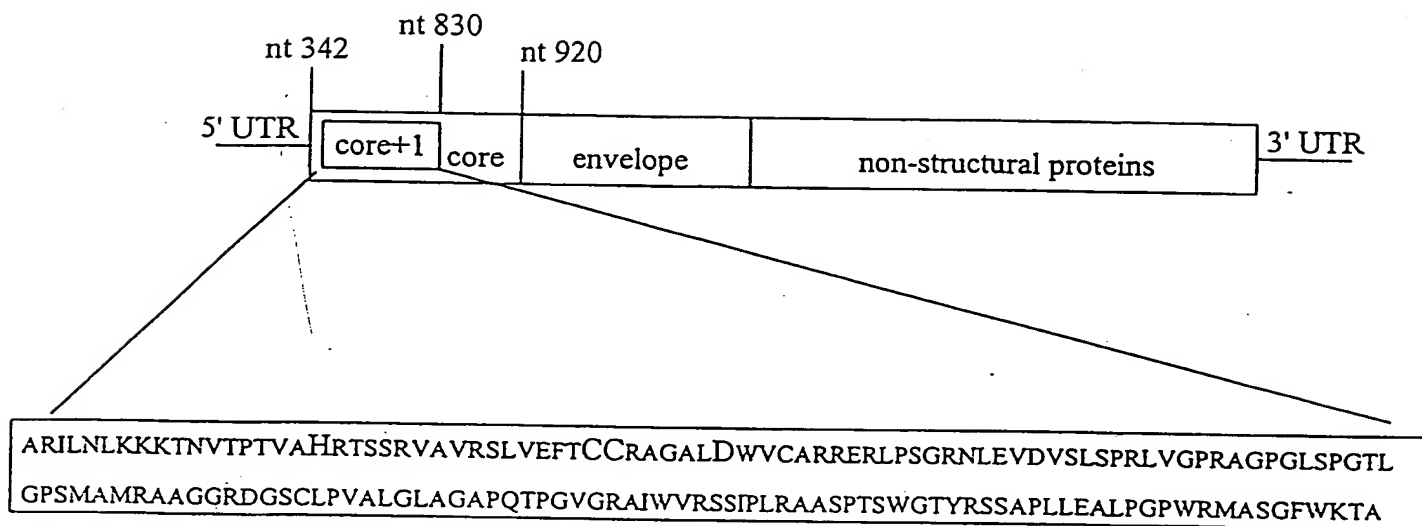


FIG. 11

Sequence Range: 342 to 840

350 360 370 380 390
* * * * *
A TGA GCA CGA ATC CTA AAC CTC AAA AAA AAA ACA AAC GTA ACA CCA ACC
T ACT CGT GCT TAG GAT TTG GAG TTT TTT TTT TGT TTG CAT TGT GGT TGG
*** Ala Arg Ile Leu Asn Leu Lys Lys Lys Thr Asn Val Thr Pro Thr>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

400 410 *putative slippery c. glut* 420 430
* * * * *
GTC GCC CAC AGG ACG TCA AGT TCC CGG GTG GCG GTC AGA TCG TTG GTG
CAG CGG GTG TCC TGC AGT TCA AGG GCC CAC CGC CAG TCT AGC AAC CAC
Val Ala His Arg Thr Ser Ser Ser Arg Val Ala Val Arg Ser Leu Val>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

440 450 460 470 480
* * * * *
GAG TTT ACT TGT TGC CGC GCA GGG GCC CTA GAT TGG GTG TGC GCG CGA
CTC AAA TGA ACA ACG GCG CGT CCC CGG GAT CTA ACC CAC ACG CGC GCT
Glu Phe Thr Cys Cys Arg Ala Gly Ala Leu Asp Trp Val Cys Ala Arg>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

490 500 510 520 530
* * * * *
CGA GAA AGA CTT CCG AGC GGT CGC AAC CTC GAG GTA GAC GTC AGC CTA
GCT CTT TCT GAA GGC TCG CCA GCG TTG GAG CTC CAT CTG CAG TCG GAT
Arg Glu Arg Leu Pro Ser Gly Arg Asn Leu Glu Val Asp Val Ser Leu>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

540 550 560 570 580
* * * * *
TCC CCA AGG CTC GTC GGC CCG AGG GCA GGA CCT GGG CTC AGC CCG GGT
AGG GGT TCC GAG CAG CCG GGC TCC CGT CCT GGA CCC GAG TCG GGC CCA
Ser Pro Arg Leu Val Gly Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

590 600 610 620 630
* * * * *
ACC CTT GGC CCC TCT ATG GCA ATG AGG GCT GCG GGT GGG CGG GAT GGC
TGG GAA CCG GGG AGA TAC CGT TAC TCC CGA CGC CCA CCC GCC CTA CCG
Thr Leu Gly Pro Ser Met Ala Met Arg Ala Ala Gly Gly Arg Asp Gly>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

640 650 660 670
* * * * *
TCC TGT CTC CCC GTG GCT CTC GGC CTA GCT GGG GCC CCA CAG ACC CCC
AGG ACA GAG GGG CAC CGA GAG CCG GAT CGA CCC CGG GGT GTC TGG GGG
Ser Cys Leu Pro Val Ala Leu Gly Leu Ala Gly Ala Pro Gln Thr Pro>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

680 690 700 710 720
* * * * *
GGC GTA GGT CGC GCA ATT TGG GTA AGG TCA TCG ATA CCC TTA CGT GCG
CCG CAT CCA GCG CGT TAA ACC CAT TCC AGT AGC TAT GGG AAT GCA CGC
Gly Val Gly Arg Ala Ile Trp Val Arg Ser Ser Ile Pro Leu Arg Ala>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

730 740 750 760 770
* * * * *
GCT TCG CCG ACC TCA TGG GGT ACA TAC CGC TCG TCG GCG CCC CTC TTG
CGA AGC GGC TGG AGT ACC CCA TGT ATG GCG AGC AGC CGC GGG GAG AAC
Ala Ser Pro Thr Ser Trp Gly Thr Tyr Arg Ser Ser Ala Pro Leu Leu>
_a_a_ TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a_a_a_>

FIGURE 12

780	790	800	810	820
* * *	* * *	* * *	* * *	* * *
GAG GCG CTG CCA GGG CCC TGG CGC ATG GCG TCC GGG TTC TGG AAG ACG				
CTC CGC GAC GGT CCC GGG ACC GCG TAC CGC AGG CCC AAG ACC TTC TGC				
Glu Ala Leu Pro Gly Pro Trp Arg Met Ala Ser Gly Phe Trp Lys Thr>				
__a__a__TRANSLATION OF ECVSEND.SEQ (RITSA) [A]_a__a__a__>				

830	840
* * *	* * *
GCG TGA ACT ATG CAA CAG	
CGC ACT TGA TAC GTT GTC	
Ala *** Thr Met Gln Gln>	
__TRANSLATION OF B__>	

FIGURE 12
(cont.)

Translation of HCP1 SEQ (Rit Annotated Sequence)

Sequence Range: 1 to 166

10	20	30	40	50	60
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
*ARILNLKKK TNVTPTVAHR TSSSRVAVRS LVEFTCCRAG ALDWVCARRE RLPSCRNLEV					
70	80	90	100	110	120
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
DVSLSPRLVG PRAGPGLSPG TLGPSMAMRA AGGRDGSCLP VALGLAGAPQ TPGVGRAIWV					
130	140	150	160		
* * * *	* * * *	* * * *	* * * *		
RSSIPLRAAS PTSWGTYRSS APLLEALPGP WRMASGTWKT A*TMQQ					

FIGURE 13